

GENOME SIGNATURE TAGS

Abstract of the Disclosure

[00181] Disclosed is a method for analyzing the organismic complexity of a sample through analysis of the nucleic acid in the sample. In the disclosed method, through a series of steps, including digestion with a type II restriction enzyme, ligation of capture adapters and linkers and digestion with a type IIS restriction enzyme, genome signature tags are produced. The sequences of a statistically significant number of the signature tags are determined and the sequences are used to identify and quantify the organisms in the sample. Various embodiments of the invention described herein include methods for using single point genome signature tags to analyze the related families present in a sample, methods for analyzing sequences associated with hyper- and hypo-methylated CpG islands, methods for visualizing organismic complexity change in a sampling location over time and methods for generating the genome signature tag profile of a sample of fragmented DNA.